GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 18, 2000, 19:10:45 ; Search time 39.33 Seconds
(without alignments)
59.490 Million cell updates/sec

Title: PCT-US97-18348-1
Perfect score: 18
Sequence: 1 CAGCGTGCGCCATCCTTC 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 230463 seqs, 64992525 residues

Total number of hits satisfying chosen parameters: 328916

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	20	2	US-08-217-082A-1	Sequence 1, Appli
c	2	18	100.0	20	2	US-08-217-082A-7	Sequence 7, Appli
	3	18	100.0	20	3	US-08-465-485A-1	Sequence 1, Appli
c	4	18	100.0	20	3	US-08-465-485A-7	Sequence 7, Appli
	5	18	100.0	20	5	US-09-080-285-1	Sequence 1, Appli
c	6	18	100.0	20	5	US-09-080-285-7	Sequence 7, Appli
c	7	18	100.0	35	2	US-08-217-082A-2	Sequence 2, Appli
c	8	18	100.0	35	3	US-08-465-485A-2	Sequence 2, Appli
c	9	18	100.0	35	5	US-09-080-285-2	Sequence 2, Appli
	10	16	88.9	17	2	US-08-217-082A-10	Sequence 10, Appl
	11	16	88.9	17	2	US-08-217-082A-11	Sequence 11, Appl
	12	13	72.2	17	2	US-08-217-082A-9	Sequence 9, Appli
	13	13	72.2	17	2	US-08-217-082A-12	Sequence 12, Appl
	14	13	72.2	18	2	US-08-217-082A-17	Sequence 17, Appl
	15	13	72.2	18	3	US-08-465-485A-17	Sequence 17, Appl
	16	13	72.2	18	3	US-08-465-485A-24	Sequence 24, Appl
	17	13	72.2	18	5	US-09-080-285-17	Sequence 17, Appl
	18	13	72.2	18	5	US-09-080-285-24	Sequence 24, Appl
c	19	13	72.2	27	1	US-08-410-804-13	Sequence 13, Appl
c	20	13	72.2	27	2	US-08-607-269-8	Sequence 8, Appli
c	21	13	72.2	27	2	US-08-259-514-13	Sequence 13, Appl
c	22	13	72.2	27	3	US-08-858-311-13	Sequence 13, Appl
c	23	13	72.2	27	6	PCT-US95-04600-8	Sequence 8, Appli
	24	12.2	67.8	30	6	PCT-US94-10257A-37	Sequence 37, Appl
	25	11.8	65.6	21	4	US-08-837-190C-1	Sequence 1, Appli
	26	11.8	65.6	21	4	US-08-837-190C-11	Sequence 11, Appl
	27	11.8	65.6	31	2	US-08-647-584-44	Sequence 44, Appl
c	28	11.8	65.6	45	1	US-07-795-859B-36	Sequence 36, Appl
c	29	11.8	65.6	45	1	US-08-457-616-36	Sequence 36, Appl
	30	11.8	65.6	48	2	US-08-741-881-41	Sequence 41, Appl
	31	11.8	65.6	48	2	US-08-739-158-41	Sequence 41, Appl
	32	11.8	65.6	48	3	US-08-739-167-41	Sequence 41, Appl
	33	11.8	65.6	48	5	US-08-404-796-41	Sequence 41, Appl
	34	11.8	65.6	48	5	US-08-931-869-41	Sequence 41, Appl
	35	11.4	63.3	25	6	PCT-US93-01852-3	Sequence 3, Appli
c	36	11.4	63.3	33	5	US-08-650-726-1	Sequence 1, Appli
c	37	11.2	62.2	47	6	PCT-US95-13552-16	Sequence 16, Appl
c	38	11.2	62.2	47	6	PCT-US95-13552-18	Sequence 18, Appl
c	39	11	61.1	19	7	5276019-8	Patent No. 5276019
	40	11	61.1	31	2	US-08-726-136-19	Sequence 19, Appl
	41	10.8	60.0	17	1	US-08-233-030-15	Sequence 15, Appl
c	42	10.8	60.0	21	5	US-08-804-439A-56	Sequence 56, Appl
c	43	10.8	60.0	21	5	US-08-720-229-56	Sequence 56, Appl
c	44	10.8	60.0	35	1	US-07-783-861C-19	Sequence 19, Appl
	45	10.8	60.0	35	1	US-07-783-861C-22	Sequence 22, Appl

ALIGNMENTS

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RESULT   1
US-08-217-082A-1
; Sequence 1, Application US/08217082A
; Patent No. 5734033
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
;    TITLE OF INVENTION:  GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  224 Airport Parkway
;      CITY:  San Jose
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  95110
;    COMPUTER READABLE FORM:
;    .  MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,082A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-067-55 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  Synthetic DNA
;    ANTI-SENSE:  YES
US-08-217-082A-1
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  Query Match             100.0%;  Score 18;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATCCTTC 18
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Db       1 CAGCGTGCGCCATCCTTC 18


RESULT   2
US-08-217-082A-7/c
; Sequence 7, Application US/08217082A
; Patent No. 5734033
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
;    TITLE OF INVENTION:  GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  224 Airport Parkway
;      CITY:  San Jose
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  95110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,082A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-067-55 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  Synthetic DNA
;    ANTI-SENSE:  NO
US-08-217-082A-7


  Query Match             100.0%;  Score 18;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATCCTTC 18
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Db      20 CAGCGTGCGCCATCCTTC 3


RESULT   3
US-08-465-485A-1
; Sequence 1, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
;   APPLICANT:  Reed, John
;   TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;   NUMBER OF SEQUENCES:  29
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;     ADDRESSEE:  P.C.
;     STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;     CITY:  Arlington
;     STATE:  Virginia
;     COUNTRY:  U.S.A.
;     ZIP:  22202
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/465,485A
;     FILING DATE:  05-JUN-1995
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/124,256
;     FILING DATE:  20-SEP-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/840,716
;     FILING DATE:  21-FEB-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/288,692
;     FILING DATE:  22-DEC-1988
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Fortney, Andrew D.
;     REGISTRATION NUMBER:  34,600
;     REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (408) 436-2070
;     TELEFAX:  (408) 436-2075
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  20 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (genomic)
;   ANTI-SENSE:  YES
US-08-465-485A-1


  Query Match             100.0%;  Score 18;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATCCTTC 18
           ||||||||||||||||||
Db       1 CAGCGTGCGCCATCCTTC 18


RESULT   4
US-08-465-485A-7/c
; Sequence 7, Application US/08465485A
; Patent No. 5831066
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
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;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,485A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
US-08-465-485A-7


  Query Match             100.0%;  Score 18;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     20 CAGCGTGCGCCATCCTTC 3


RESULT   5
US-09-080-285-1
; Sequence 1, Application US/09080285
; Patent No. 6040181
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/080,285
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/465,485
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  YES
US-09-080-285-1


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  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
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Db      1 CAGCGTGCGCCATCCTTC 18


RESULT   6
US-09-080-285-7/c
; Sequence 7, Application US/09080285
; Patent No. 6040181
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/080,285
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/465,485
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
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;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
US-09-080-285-7


  Query Match             100.0%;  Score 18;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     20 CAGCGTGCGCCATCCTTC 3


RESULT   7
US-08-217-082A-2/c
; Sequence 2, Application US/08217082A
; Patent No. 5734033
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
;    TITLE OF INVENTION:  GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  224 Airport Parkway
;      CITY:  San Jose
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  95110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,082A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-067-55 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    ANTI-SENSE:  NO
US-08-217-082A-2


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  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
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Db     30 CAGCGTGCGCCATCCTTC 13


RESULT   8
US-08-465-485A-2/c
; Sequence 2, Application US/08465485A
; Patent No. 5831066
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,485A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
US-08-465-485A-2


  Query Match             100.0%;  Score 18;  DB 3;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     30 CAGCGTGCGCCATCCTTC 13
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RESULT  9
US-09-080-285-2/c
; Sequence 2, Application US/09080285
; Patent No. 6040181
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/080,285
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/465,485
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
US-09-080-285-2


  Query Match             100.0%;  Score 18;  DB 5;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATCCTTC 18
           ||||||||||||||||||
Db      30 CAGCGTGCGCCATCCTTC 13


RESULT  10
US-08-217-082A-10
; Sequence 10, Application US/08217082A
; Patent No. 5734033
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
;    TITLE OF INVENTION:  GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  224 Airport Parkway
;      CITY:  San Jose
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  95110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,082A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-067-55 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  Synthetic DNA
;    ANTI-SENSE:  YES
US-08-217-082A-10


  Query Match             88.9%;  Score 16;  DB 2;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATCCT 16
           ||||||||||||||||
Db       2 CAGCGTGCGCCATCCT 17


RESULT  11
US-08-217-082A-11
; Sequence 11, Application US/08217082A
; Patent No. 5734033
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
;    TITLE OF INVENTION:  GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  224 Airport Parkway
;      CITY:  San Jose
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  95110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,082A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-067-55 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  Synthetic DNA
;    ANTI-SENSE:  YES
US-08-217-082A-11


  Query Match             88.9%;  Score 16;  DB 2;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCGTGCGCCATCCTTC 18
           ||||||||||||||||
Db       1 GCGTGCGCCATCCTTC 16


RESULT  12
US-08-217-082A-9
; Sequence 9, Application US/08217082A
; Patent No. 5734033
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
;    TITLE OF INVENTION:  GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  224 Airport Parkway
;      CITY:  San Jose
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  95110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,082A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-067-55 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  Synthetic DNA
;    ANTI-SENSE:  YES
US-08-217-082A-9


  Query Match             72.2%;  Score 13;  DB 2;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCAT 13
           |||||||||||||
Db       5 CAGCGTGCGCCAT 17


RESULT  13
US-08-217-082A-12
; Sequence 12, Application US/08217082A
; Patent No. 5734033
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
;    TITLE OF INVENTION:  GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  224 Airport Parkway
;      CITY:  San Jose
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  95110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,082A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-067-55 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
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;      DESCRIPTION:  Synthetic DNA
;    ANTI-SENSE:  YES
US-08-217-082A-12


  Query Match             72.2%;  Score 13;  DB 2;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 TGCGCCATCCTTC 18
          |||||||||||||
Db      1 TGCGCCATCCTTC 13


RESULT  14
US-08-217-082A-17
; Sequence 17, Application US/08217082A
; Patent No. 5734033
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
;    TITLE OF INVENTION:  GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  224 Airport Parkway
;      CITY:  San Jose
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  95110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,082A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-067-55 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  Synthetic DNA
US-08-217-082A-17


  Query Match             72.2%;  Score 13;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCAT 13
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Db      6 CAGCGTGCGCCAT 18


RESULT  15
US-08-465-485A-17
; Sequence 17, Application US/08465485A
; Patent No. 5831066
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,485A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-465-485A-17


  Query Match             72.2%;  Score 13;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCAT 13
          |||||||||||||
Db      6 CAGCGTGCGCCAT 18


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GenCore version 4.5

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76: /cgn2_6/ptodata/2/pna/US6009B_COMB.seq:*
77: /cgn2_6/ptodata/2/pna/US6010A_COMB.seq:*
78: /cgn2_6/ptodata/2/pna/US6010B_COMB.seq:*
79: /cgn2_6/ptodata/2/pna/US6011A_COMB.seq:*
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81: /cgn2_6/ptodata/2/pna/US6012A_COMB.seq:*
82: /cgn2_6/ptodata/2/pna/US6012B_COMB.seq:*
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84: /cgn2_6/ptodata/2/pna/US6013B_COMB.seq:*
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86: /cgn2_6/ptodata/2/pna/US6014B_COMB.seq:*
87: /cgn2_6/ptodata/2/pna/US6014C_COMB.seq:*
88: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
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90: /cgn2_6/ptodata/2/pna/US6016B_COMB.seq:*
91: /cgn2_6/ptodata/2/pna/US6016C_COMB.seq:*
92: /cgn2_6/ptodata/2/pna/US6017A_COMB.seq:*
93: /cgn2_6/ptodata/2/pna/US6017B_COMB.seq:*
94: /cgn2_6/ptodata/2/pna/US6017C_COMB.seq:*
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96: /cgn2_6/ptodata/2/pna/US6018B_COMB.seq:*
97: /cgn2_6/ptodata/2/pna/US6018C_COMB.seq:*
98: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
99: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
100: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
101: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
102: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
103: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
104: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	1	PCT-US97-18348-1	Sequence 1, Appli
	2	18	100.0	18	19	US-08-726-211-1	Sequence 1, Appli
c	3	18	100.0	20	1	PCT-US94-10725-7	Sequence 7, Appli

c	4	18	100.0	20	5	US-08-124-256-7	Sequence 7, Appli
c	5	18	100.0	20	9	US-08-217-082-7	Sequence 7, Appli
	6	18	100.0	20	52	US-09-379-718-1	Sequence 1, Appli
c	7	18	100.0	20	52	US-09-379-718-2	Sequence 2, Appli
	8	18	100.0	20	57	US-09-506-979-1	Sequence 1, Appli
	9	18	100.0	22	14	US-08-403-721-3	Sequence 3, Appli
	10	18	100.0	22	14	US-08-403-721-4	Sequence 4, Appli
	11	18	100.0	22	16	US-08-472-801-304	Sequence 304, App
	12	18	100.0	22	18	US-08-668-235-305	Sequence 305, App
c	13	18	100.0	35	1	PCT-US94-10725-2	Sequence 2, Appli
c	14	18	100.0	35	5	US-08-124-256-2	Sequence 2, Appli
c	15	18	100.0	35	9	US-08-217-082-2	Sequence 2, Appli
	16	18	100.0	45	16	US-08-472-801-303	Sequence 303, App
	17	18	100.0	45	18	US-08-668-235-304	Sequence 304, App
	18	17	94.4	19	35	US-09-018-194-7	Sequence 7, Appli
	19	14	77.8	15	57	US-09-506-979-8	Sequence 8, Appli
	20	13.8	76.7	46	54	US-09-404-520-40525	Sequence 40525, A
c	21	13.2	73.3	20	57	US-09-514-000-13846	Sequence 13846, A
	22	13	72.2	15	57	US-09-506-979-9	Sequence 9, Appli
	23	13	72.2	18	1	PCT-US94-10725-17	Sequence 17, Appl
	24	13	72.2	18	1	PCT-US97-19791-45	Sequence 45, Appl
	25	13	72.2	18	1	PCT-US99-09863-49	Sequence 49, Appl
	26	13	72.2	18	1	PCT-US99-09863-89	Sequence 89, Appl
	27	13	72.2	18	5	US-08-124-256-17	Sequence 17, Appl
	28	13	72.2	18	19	US-08-738-652A-55	Sequence 55, Appl
	29	13	72.2	18	19	US-08-738-652-55	Sequence 55, Appl
	30	13	72.2	18	31	US-08-960-774-45	Sequence 45, Appl
	31	13	72.2	18	36	US-09-030-701-27	Sequence 27, Appl
	32	13	72.2	18	38	US-09-078-954-14	Sequence 14, Appl
	33	13	72.2	18	38	US-09-078-955-14	Sequence 14, Appl
	34	13	72.2	18	40	US-09-108-673A-34	Sequence 34, Appl
	35	13	72.2	18	40	US-09-118-220-1	Sequence 1, Appli
	36	13	72.2	18	42	US-09-191-170-53	Sequence 53, Appl
	37	13	72.2	18	44	US-09-241-653-62	Sequence 62, Appl
	38	13	72.2	18	44	US-09-249-247-218	Sequence 218, App
	39	13	72.2	18	44	US-09-249-730-218	Sequence 218, App
	40	13	72.2	18	46	US-09-286-098-59	Sequence 59, Appl
	41	13	72.2	18	46	US-09-286-098-104	Sequence 104, App
	42	13	72.2	18	48	US-09-306-281-49	Sequence 49, Appl
	43	13	72.2	18	48	US-09-306-281-89	Sequence 89, Appl
	44	13	72.2	18	49	US-09-337-584-45	Sequence 45, Appl
	45	13	72.2	18	102	US-08-923-771B-146	Sequence 146, App

ALIGNMENTS

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RESULT   1
PCT-US97-18348-1
; Sequence 1, Application PC/TUS9718348
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY
;    TITLE OF INVENTION:  LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES
;    NUMBER OF SEQUENCES:  7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US97/18348
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/726,211
;      FILING DATE:  04-OCT-1996
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US97-18348-1


  Query Match             100.0%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      1 CAGCGTGCGCCATCCTTC 18


RESULT   2
US-08-726-211-1
; Sequence 1, Application US/08726211
;  GENERAL INFORMATION:
;    APPLICANT:  Tormo, Mar
;    APPLICANT:  Tari, Ana M.
;    APPLICANT:  Lopez-Berestein, Gabriel
;    TITLE OF INVENTION:  INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY
;    TITLE OF INVENTION:  LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/726,211
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  UTXC:504
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-726-211-1


  Query Match             100.0%;  Score 18;  DB 19;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      1 CAGCGTGCGCCATCCTTC 18


RESULT   3
PCT-US94-10725-7/c
; Sequence 7, Application PC/TUS9410725
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gray Cary Ware & Freidenrich
;      STREET:  401 B Street, Suite 1700
```

```
;       CITY:  San Diego
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92101-4297
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette 3.5 inch, 1.44 Mb storage
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/10725
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brotman, Harris F.
;       REGISTRATION NUMBER:  35461
;       REFERENCE/DOCKET NUMBER:  P0040WO1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 699-3630
;       TELEFAX:  (619) 236-1048
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     ANTI-SENSE:  NO
PCT-US94-10725-7


  Query Match             100.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     20 CAGCGTGCGCCATCCTTC 3


RESULT   4
US-08-124-256-7/c
; Sequence 7, Application US/08124256
;  GENERAL INFORMATION:
;     APPLICANT:  Reed, John
;     TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Gray, Cary, Ames & Frye
;       STREET:  401 B Street, Suite 1700
;       CITY:  San Diego
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92101-4297
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/124,256
;       FILING DATE:
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brotman, Harris F.
;       REGISTRATION NUMBER:  35461
;       REFERENCE/DOCKET NUMBER:  P0041US0
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 699-3630
;       TELEFAX:  (619) 236-1048
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     ANTI-SENSE:  NO
US-08-124-256-7


  Query Match             100.0%;  Score 18;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     20 CAGCGTGCGCCATCCTTC 3


RESULT   5
US-08-217-082-7/c
; Sequence 7, Application US/08217082
;  GENERAL INFORMATION:
;     APPLICANT:  John Reed
;     TITLE OF INVENTION:  Antisense Oligonucleotides For
;     TITLE OF INVENTION:  Inhibiting the Growth of Cells Expressing the
;     TITLE OF INVENTION:  Human bcl-2 Gene
;     NUMBER OF SEQUENCES:  16
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Woodcock Washburn Kurtz
;       ADDRESSEE:  Mackiewicz & Norris
;       STREET:  One Liberty Place - 46th Floor
;       CITY:  Philadelphia
;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19103
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  PC-DOS
;       SOFTWARE:  WORDPERFECT 5.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/217,082
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/840,716
;       FILING DATE:
;       APPLICATION NUMBER:  288,692
;       FILING DATE:  December 22, 1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jane Massey Licata
;       REGISTRATION NUMBER:  32,257
;       REFERENCE/DOCKET NUMBER:  UPN-0906
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-3100
;       TELEFAX:  (215) 568-3439
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     ANTI-SENSE:  No
US-08-217-082-7


  Query Match             100.0%;  Score 18;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     20 CAGCGTGCGCCATCCTTC 3
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RESULT   6
US-09-379-718-1
; Sequence 1, Application US/09379718
; GENERAL INFORMATION:
;  APPLICANT: Farrell, Nicholas
;  APPLICANT: Kloster, Miriam
;  TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
;  TITLE OF INVENTION: Antisense Technology
;  FILE REFERENCE: farrell/kloster
;  CURRENT APPLICATION NUMBER: US/09/379,718
;  CURRENT FILING DATE: 1999-08-24
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: oligonucleotides for gene therapy
US-09-379-718-1


  Query Match             100.0%;  Score 18;  DB 52;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      1 cagcgtgcgccatccttc 18


RESULT   7
US-09-379-718-2/c
; Sequence 2, Application US/09379718
; GENERAL INFORMATION:
;  APPLICANT: Farrell, Nicholas
;  APPLICANT: Kloster, Miriam
;  TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
;  TITLE OF INVENTION: Antisense Technology
;  FILE REFERENCE: farrell/kloster
;  CURRENT APPLICATION NUMBER: US/09/379,718
;  CURRENT FILING DATE: 1999-08-24
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: oligonucleotides for gene therapy
US-09-379-718-2


  Query Match             100.0%;  Score 18;  DB 52;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     20 CAGCGTGCGCCATCCTTC 3


RESULT   8
US-09-506-979-1
; Sequence 1, Application US/09506979
; GENERAL INFORMATION:
;  APPLICANT: TARI, ANA M.
;  APPLICANT: LOPEZ-BERESTEIN, GABRIEL
;  APPLICANT: GUTIERREZ-PUENTE, YOLANDA
;  TITLE OF INVENTION: SMALL OLIGONUCLEOTIDES WITH ANTI-TUMOR ACTIVITY
;  FILE REFERENCE: UTXC619
;  CURRENT APPLICATION NUMBER: US/09/506,979
;  CURRENT FILING DATE: 2000-02-18
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-506-979-1


  Query Match             100.0%;  Score 18;  DB 57;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      1 cagcgtgcgccatccttc 18


RESULT   9
US-08-403-721-3
; Sequence 3, Application US/08403721
;  GENERAL INFORMATION:
;    APPLICANT:  EVAN, Gerald Ian
;    TITLE OF INVENTION:  Modified Cells And Methods Of Treatment
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HALE and DORR
;      STREET:  1455 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,721
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/00686
;      FILING DATE:  02 APRIL 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HENRY N. WIXON
;      REFERENCE/DOCKET NUMBER:  104322.139
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 942-8400
;      TELEFAX:  (202) 942-8484
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-403-721-3


  Query Match             100.0%;  Score 18;  DB 14;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      3 CAGCGTGCGCCATCCTTC 20


RESULT  10
US-08-403-721-4
; Sequence 4, Application US/08403721
;  GENERAL INFORMATION:
;    APPLICANT:  EVAN, Gerald Ian
;    TITLE OF INVENTION:  Modified Cells And Methods Of Treatment
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HALE and DORR
;      STREET:  1455 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,721
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/00686
;      FILING DATE:  02 APRIL 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HENRY N. WIXON
;      REFERENCE/DOCKET NUMBER:  104322.139
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 942-8400
;      TELEFAX:  (202) 942-8484
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-403-721-4


  Query Match             100.0%;  Score 18;  DB 14;  Length 22;
  Best Local Similarity   77.8%;  Pred. No. 12;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          |||||:||||||:||::|
Db      3 CAGCGUGCGCCAUCCUUC 20


RESULT  11
US-08-472-801-304
; Sequence 304, Application US/08472801
; GENERAL INFORMATION:
;  APPLICANT: Hesed 2
;  APPLICANT: Smith, Larry J.
;  TITLE OF INVENTION: Method and Compositions for Cellular
;  TITLE OF INVENTION: Reprogramming
;  FILE REFERENCE: Hesed 2
;  CURRENT APPLICATION NUMBER: US/08/472,801
;  CURRENT FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 3601
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 304
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-472-801-304


  Query Match             100.0%;  Score 18;  DB 16;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      3 cagcgtgcgccatccttc 20


RESULT  12
US-08-668-235-305
; Sequence 305, Application US/08668235
; GENERAL INFORMATION:
;  APPLICANT: Larry J. Smith
;  TITLE OF INVENTION: Methods and Compositions for Cellular
;  TITLE OF INVENTION: Reprogramming
;  FILE REFERENCE: Hesed-1
;  CURRENT APPLICATION NUMBER: US/08/668,235
;  CURRENT FILING DATE: 1996-06-17
;  EARLIER APPLICATION NUMBER: 07/748,997
;  EARLIER FILING DATE: 08/23/91
;  EARLIER APPLICATION NUMBER: 08/426,781
;  EARLIER FILING DATE: 04/22/95
;  EARLIER APPLICATION NUMBER: 08/472,801
;  EARLIER FILING DATE: 06/07/95
;  NUMBER OF SEQ ID NOS: 3629
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 305
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-668-235-305


  Query Match             100.0%;  Score 18;  DB 18;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      3 cagcgtgcgccatccttc 20


RESULT  13
PCT-US94-10725-2/c
; Sequence 2, Application PC/TUS9410725
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gray Cary Ware & Freidenrich
;      STREET:  401 B Street, Suite 1700
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92101-4297
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette 3.5 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10725
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Brotman, Harris F.
;       REGISTRATION NUMBER:  35461
;       REFERENCE/DOCKET NUMBER:  P0040WO1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 699-3630
;       TELEFAX:  (619) 236-1048
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  35 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     ANTI-SENSE:  NO
PCT-US94-10725-2


  Query Match             100.0%;  Score 18;  DB 1;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATCCTTC 18
           ||||||||||||||||||
Db      30 CAGCGTGCGCCATCCTTC 13


RESULT  14
US-08-124-256-2/c
; Sequence 2, Application US/08124256
;  GENERAL INFORMATION:
;     APPLICANT:  Reed, John
;     TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Gray, Cary, Ames & Frye
;       STREET:  401 B Street, Suite 1700
;       CITY:  San Diego
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92101-4297
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/124,256
;       FILING DATE:
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brotman, Harris F.
;       REGISTRATION NUMBER:  35461
;       REFERENCE/DOCKET NUMBER:  P0041US0
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 699-3630
;       TELEFAX:  (619) 236-1048
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  35 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     ANTI-SENSE:  NO
US-08-124-256-2


  Query Match             100.0%;  Score 18;  DB 5;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATCCTTC 18
           ||||||||||||||||||
Db      30 CAGCGTGCGCCATCCTTC 13


RESULT  15
US-08-217-082-2/c
; Sequence 2, Application US/08217082
;  GENERAL INFORMATION:
;     APPLICANT:  John Reed
;     TITLE OF INVENTION:  Antisense Oligonucleotides For
;     TITLE OF INVENTION:  Inhibiting the Growth of Cells Expressing the
;     TITLE OF INVENTION:  Human bcl-2 Gene
;     NUMBER OF SEQUENCES:  16
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Woodcock Washburn Kurtz
;       ADDRESSEE:  Mackiewicz & Norris
;       STREET:  One Liberty Place - 46th Floor
;       CITY:  Philadelphia
;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19103
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  PC-DOS
;       SOFTWARE:  WORDPERFECT 5.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/217,082
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/840,716
;       FILING DATE:
;       APPLICATION NUMBER:  288,692
;       FILING DATE:  December 22, 1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jane Massey Licata
;       REGISTRATION NUMBER:  32,257
;       REFERENCE/DOCKET NUMBER:  UPN-0906
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-3100
;       TELEFAX:  (215) 568-3439
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  35
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     ANTI-SENSE:  No
US-08-217-082-2


  Query Match             100.0%;  Score 18;  DB 9;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATCCTTC 18
           ||||||||||||||||||
Db      30 CAGCGTGCGCCATCCTTC 13


Search completed: June 18, 2000, 21:25:09
Job time: 3270 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 18, 2000, 18:33:40 ; Search time 525.5 Seconds
(without alignments)
138.835 Million cell updates/sec

Title: PCT-US97-18348-1
Perfect score: 18
Sequence: 1 CAGCGTGCGCCATCCTTC 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 23194

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
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32: gb_est13:*
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42: gb_est23:*
43: gb_est24:*
44: gb_est25:*
45: gb_est26:*
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49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
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57: em_est25:*
58: em_est26:*
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60: gb_est34:*
61: gb_est35:*
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65: em_est27:*
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74: gb_est44:*
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82: gb_gss1:*
83: gb_gss2:*
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90: gb_gss5:*
91: gb_gss6:*
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93: gb_gss8:*
94: gb_gss9:*
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96: em_gss6:*
97: em_gss7:*
98: em_gss8:*
99: em_gss9:*
100: em_gss10:*
101: em_gss11:*
102: gb_gss10:*
103: gb_gss11:*
104: em_gss12:*
105: gb_gss12:*
106: gb_gss13:*
107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query

	No.	Score	Match Length	DB	ID	Description
c	1	11.8	65.6 25	40	AA961707	AA961707 or40e08.s
c	2	11.6	64.4 41	37	AA680963	AA680963 LmFrAm057
	3	10.8	60.0 35	23	H53677	H53677 yu38f01.r1
c	4	10.8	60.0 43	41	AI038493	AI038493 ox38a09.s
c	5	10.8	60.0 49	20	T11453	T11453 CHR90019 Ch
	6	10.6	58.9 37	43	AI188871	AI188871 qd27b11.x
c	7	10.2	56.7 31	46	AI459772	AI459772 ao93c06.x
	8	10.2	56.7 40	46	AI459438	AI459438 ar81b11.x
c	9	10.2	56.7 43	36	AA654543	AA654543 nt59d05.s
	10	10.2	56.7 43	40	AI000393	AI000393 ot06e05.s
	11	10.2	56.7 46	39	AA854777	AA854777 aj77b02.s
	12	10	55.6 31	39	AA868659	AA868659 ak49g02.s
c	13	10	55.6 41	34	AA509356	AA509356 vg18a09.r
	14	10	55.6 45	94	AQ025518	AQ025518 EP(X)1587
c	15	10	55.6 49	44	AI254752	AI254752 qt89f07.x
c	16	10	55.6 49	49	AI628197	AI628197 ty22f08.x
c	17	9.8	54.4 26	94	AQ025266	AQ025266 EP(3)3084
c	18	9.8	54.4 28	48	AI625245	AI625245 ts42e06.x
c	19	9.8	54.4 34	26	W24112	W24112 zb48h04.r1
	20	9.8	54.4 37	38	AA808573	AA808573 ob38b02.s
	21	9.8	54.4 37	82	HSMC09A10	X88437 H.sapiens D
	22	9.8	54.4 40	30	AA226145	AA226145 nc09f09.r
	23	9.8	54.4 43	30	AA231183	AA231183 mw33f06.r
c	24	9.8	54.4 48	21	T61673	T61673 yb87g04.s1
	25	9.6	53.3 34	40	AA971412	AA971412 op92c11.s
c	26	9.6	53.3 34	47	AI528944	AI528944 ud43c06.y
	27	9.6	53.3 37	39	AA867149	AA867149 vx23h09.r
c	28	9.6	53.3 40	24	H99190	H99190 yx15d07.s1
	29	9.6	53.3 43	40	AA948558	AA948558 on68d08.s
c	30	9.6	53.3 43	44	AI282449	AI282449 qv04c12.x
	31	9.6	53.3 46	37	AA719000	AA719000 zh22h04.s
	32	9.6	53.3 49	38	AA795140	AA795140 vq94b01.r
	33	9.6	53.3 49	38	AA813812	AA813812 ai72c08.s
c	34	9.6	53.3 49	44	AI246743	AI246743 qk40c09.x
c	35	9.4	52.2 34	41	AI020003	AI020003 ua95h03.r
	36	9.4	52.2 37	39	AA889248	AA889248 ak26d11.s
c	37	9.4	52.2 40	41	AI027584	AI027584 ow40a04.x
c	38	9.4	52.2 43	22	H09843	H09843 ym01d05.r1
	39	9.4	52.2 43	33	AA433628	AA433628 vf47d01.r
c	40	9.4	52.2 46	23	H49581	H49581 yo23b02.s1
	41	9.4	52.2 46	34	AA455514	AA455514 zx77g01.s
	42	9.4	52.2 47	23	R85311	R85311 yo39d07.r1
c	43	9.4	52.2 49	26	W40572	W40572 zc79e12.r1
	44	9.4	52.2 49	30	AA233183	AA233183 zr69f08.s
c	45	9.2	51.1 27	22	R23703	R23703 yh35e11.r1

ALIGNMENTS

```
RESULT   1
AA961707/c
LOCUS       AA961707       25 bp    mRNA            EST       27-AUG-1998
DEFINITION  or40e08.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1598342 3'
            similar to SW:SN24_HUMAN P51532 POSSIBLE GLOBAL TRANSCRIPTION
            ACTIVATOR SNF2L4 ;contains TAR1.t2 TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION   AA961707
VERSION     AA961707.1  GI:3133871
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407458.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Insert Length: 388   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1598342"
                     /clone_lib="NCI_CGAP_GC3"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is not normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        4 a      7 c     10 g      4 t
ORIGIN


  Query Match             65.6%;  Score 11.8;  DB 40;  Length 25;
  Best Local Similarity   86.7%;  Pred. No. 1.3e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCC 15
          ||||||||| || ||
Db     24 CAGCGTGCGTCAACC 10


RESULT   2
AA680963/c
LOCUS       AA680963       41 bp    mRNA            EST       09-DEC-1998
DEFINITION  LmFrAm0579 Leishmania major Amastigote Lambda Zap II library
            Leishmania major cDNA clone S07 5', mRNA sequence.
ACCESSION   AA680963
VERSION     AA680963.1  GI:2662968
KEYWORDS    EST.
SOURCE      Leishmania major.
  ORGANISM  Leishmania major
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Leishmania.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Norrish,A.R., Dyall,S.D., Smith,D.F. and Blackwell,J.M.
  TITLE     Analysis of Leishmania Major Amastigote Expressed Sequence Tags
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1997 this sequence version replaced gi:2264545.
            Contact: Blackwell JM
            Cambridge Institute for Medical Research
            Wellcome Trust/MRC Building, Addenbrooke's Hospital, Hills Road,
            Cambridge CB2 2XY, UK
            Tel: 01223 336 143
            Fax: 01223 331 206
            Email: jmb37@cus.cam.ac.uk
            PCR PRimers
            FORWARD: GTAAAACGACGGCCAGT
            BACKWARD: GGAAACAGCTATGACCATG
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
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     source          1. .41
                     /organism="Leishmania major"
                     /strain="Friedlin"
                     /db_xref="taxon:5664"
                     /clone="S07"
                     /clone_lib="Leishmania major Amastigote Lambda Zap II
                     library"
                     /cell_type="Amastigote"
                     /note="Vector: Lambda Zap II; Site_1: Xho1; Site_2: Not1"
BASE COUNT        9 a     14 c      8 g     10 t
ORIGIN


  Query Match             64.4%;  Score 11.6;  DB 37;  Length 41;
  Best Local Similarity   77.8%;  Pred. No. 1.9e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||| ||||| |||  |||
Db     29 CAGAGTGCGACATGATTC 12


RESULT   3
H53677
LOCUS       H53677          35 bp    mRNA            EST       20-SEP-1995
DEFINITION  yu38f01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:236089 5' similar to gb:X01683 ALPHA-1-ANTITRYPSIN PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   H53677
VERSION     H53677.1  GI:993824
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
            Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
            and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     On May 8, 1995 this sequence version replaced gi:800757.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 1505
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 1505    Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .35
                      /organism="Homo sapiens"
                      /db_xref="GDB:3863008"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:236089"
                      /clone_lib="Soares ovary tumor NbHOT"
                      /sex="Female"
                      /tissue_type="ovarian tumor"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was size selected, ligated to Eco RI
                      adapters (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of a modified pT7T3 vector
                      (Pharmacia). Library constructed by Bento Soares and
                      M.Fatima Bonaldo. "
BASE COUNT        3 a     11 c      9 g     11 t      1 others
ORIGIN


  Query Match             60.0%;  Score 10.8;  DB 23;  Length 35;
  Best Local Similarity   80.0%;  Pred. No. 4.5e+04;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      4 CGTGCGCCATCCTTC 18
          |||| | ||||||  |
Db     19 CGTGGGGCATCCTNC 33


RESULT   4
AI038493/c
LOCUS       AI038493        43 bp    mRNA            EST       24-SEP-1998
DEFINITION  ox38a09.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
            IMAGE:1658584 3' similar to TR:Q41707 Q41707 EXTENSIN CLASS 1
            PROTEIN PRECURSOR. ;, mRNA sequence.
ACCESSION   AI038493
VERSION     AI038493.1  GI:3277687
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 5, 1995 this sequence version replaced gi:797645.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 332    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .43
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1658584"
                      /clone_lib="Soares_total_fetus_Nb2HF8_9w"
                      /dev_stage="8-9 weeks"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was prepared from mRNA obtained from pooled 8-9 week
                      (total) fetus material with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCTTAATTTTTTTTTTTTTTTT 3'].
                      Double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. Library
                      went through one round of normalization, and was
                      constructed  by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       11 a      6 c     24 g      2 t
ORIGIN


  Query Match             60.0%;  Score 10.8;  DB 41;  Length 43;
```

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  Best Local Similarity   85.7%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 CGTGCGCCATCCTT 17
           ||||| ||||| ||
Db      14 CGTGCTCCATCGTT 1


RESULT   5
T11453/c
LOCUS       T11453          49 bp    DNA             EST       30-NOV-1993
DEFINITION  CHR90019 Chromosome 9 exon Homo sapiens genomic clone 34B-5 5' and
            3', mRNA sequence.
ACCESSION   T11453
VERSION     T11453.1  GI:430876
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Church,D.M., Banks,L.T., Rogers,A.C., Graw,S.L., Housman,D.E.,
            Gusella,J.F. and Buckler,A.J.
  TITLE     Identification of human chromosome 9 specific genes using exon
            amplification
  JOURNAL   Hum. Mol. Genet. 2, 1915-1920 (1993)
  MEDLINE   94108448
COMMENT     Contact: Buckler AJ
            Molecular Neurogenetics Unit
            Massachusetts General Hospital
            Building 149, 13th St., Charlestown MA 02129
            Tel: 6177249616
            Fax: 6177265736
            Email: buckler@helix.mgh.harvard.edu
            Seq primer: T3 and T7.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="34B-5"
                     /clone_lib="Chromosome 9 exon"
                     /lab_host="E. Coli DH5a"
                     /note="Vector: pBluescriptIIKS+; Exons were isolated from
                     human chromosome 9 specific cosmids using the method of
                     exon amplification (Proc. Natl. Acad. Sci USA
                     88:4005-4009, 1991).  Exons were cloned into
                     pBluescriptIIKS+ converted to T vector at the EcoRV site.
                     "
BASE COUNT       14 a      6 c     18 g     11 t
ORIGIN


  Query Match             60.0%;  Score 10.8;  DB 20;  Length 49;
  Best Local Similarity   85.7%;  Pred. No. 4.9e+04;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATC 14
           |||| ||| |||||
Db      19 CAGCTTGCTCCATC 6


RESULT   6
AI188871
LOCUS       AI188871        37 bp    mRNA            EST       13-OCT-1998
DEFINITION  qd27b11.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:1724925 3' similar to SW:POR2_HUMAN P45880
            VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2 ;, mRNA
            sequence.
ACCESSION   AI188871
VERSION     AI188871.1  GI:3740080
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1724925"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT       8 a      12 c      9 g      8 t
ORIGIN


  Query Match             58.9%;  Score 10.6;  DB 43;  Length 37;
  Best Local Similarity   76.5%;  Pred. No. 5.7e+04;
  Matches   13;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATCCTT 17
           ||| | | |||| ||||
Db      15 CAGGGCGAGCCAACCTT 31


RESULT   7
AI459772/c
LOCUS       AI459772        31 bp    mRNA            EST       09-MAR-1999
DEFINITION  ao93c06.x1 Schiller meningioma Homo sapiens cDNA clone
            IMAGE:1953418 3' similar to SW:NUBM_BOVIN P25708 NADH-UBIQUINONE
            OXIDOREDUCTASE 51 KD SUBUNIT PRECURSOR ;, mRNA sequence.
ACCESSION   AI459772
VERSION     AI459772.1  GI:4312653
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3188933.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
```

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            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1953418"
                     /clone_lib="Schiller meningioma"
                     /sex="female"
                     /tissue_type="meningioma"
                     /dev_stage="72 years"
                     /lab_host="SOLR"
                     /note="Organ: brain; Vector: pBluescript SK- (Stratagene);
                     Site_1: EcoRI; Site_2: XhoI; Double-stranded cDNA was
                     prepared from human meningioma using primer
                     5'-GAGAGAGAGAGAGAGAGAGAAACTAGTCTGAGT(18)-3'.  An EcoRI
                     adaptor was used on the 5' end of the cDNA as follows:
                     5'-AATTCGGCACGAG-3'.  The library was size-selected and
                     went through one round of amplification.  Average insert
                     size is 1.7 kb, with a range from 0.4-12 kb.  Tumor
                     identification by  consensus pathology. This library was
                     constructed by Dr. Martin Schiller (Johns Hopkins
                     University)."
BASE COUNT        7 a      11 c      7 g      6 t
ORIGIN


  Query Match             56.7%;  Score 10.2;  DB 46;  Length 31;
  Best Local Similarity   80.0%;  Pred. No. 8.6e+04;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCATCC 15
           ||| || |||||| |
Db      22 CAGTGTACGCCATGC 8


RESULT   8
AI459438
LOCUS       AI459438       40 bp    mRNA            EST       09-MAR-1999
DEFINITION  ar81b11.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone
            IMAGE:2151645 3' similar to SW:COX3_HYLLA Q95707 CYTOCHROME C
            OXIDASE POLYPEPTIDE III ;, mRNA sequence.
ACCESSION   AI459438
VERSION     AI459438.1  GI:4312319
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3188598.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2151645"
                     /clone_lib="Barstead colon HPLRB7"
                     /sex="male"
                     /dev_stage="adult, age 25"
                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTT
                     3'];  double-stranded cDNA was ligated to Eco RI adaptors
                     [5' AATTCACTAGTAAT 3' and 5' ATTACTAGTG 3'],  digested
                     with Not I and cloned into the Not I and Eco RI sites of
                     the modified pT7T3 vector. Library constructed by Bob
                     Barstead."
BASE COUNT        6 a      9 c      15 g     10 t
ORIGIN


  Query Match             56.7%;  Score 10.2;  DB 46;  Length 40;
  Best Local Similarity   80.0%;  Pred. No. 9.2e+04;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 AGCGTGCGCCATCCT 16
           |||  | ||||||||
Db      12 AGCCAGTGCCATCCT 26


RESULT   9
AA654543/c
LOCUS       AA654543       43 bp    mRNA            EST       04-NOV-1997
DEFINITION  nt59d05.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1202793
            similar to SW:RS19_HUMAN P39019 40S RIBOSOMAL PROTEIN S19. [1] ;,
            mRNA sequence.
ACCESSION   AA654543
VERSION     AA654543.1  GI:2590697
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393535.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
            M.D., Michael Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1202793"
                     /clone_lib="NCI_CGAP_Pr3"
                     /sex="Male"
                     /dev_stage="45 years old"
```

/lab_host="DH10B"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
BASE COUNT 8 a 11 c 12 g 12 t
ORIGIN

Query Match 56.7%; Score 10.2; DB 36; Length 43;
Best Local Similarity 80.0%; Pred. No. 9.4e+04;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCGTGCGCCATCC 15
|||| ||| |||| |
Db 22 CAGCTTGCTCCATAC 8

RESULT 10
AI000393
LOCUS AI000393 43 bp mRNA EST 13-FEB-1999
DEFINITION ot06e05.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1614080 3' similar to TR:O00409 O00409 CHECKPOINT SUPPRESSOR 1. ;, mRNA sequence.
ACCESSION AI000393
VERSION AI000393.1 GI:3190947
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044803.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1173 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .43
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1614080"
/clone_lib="NCI_CGAP_GC3"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 7 a 12 c 15 g 9 t
ORIGIN

Query Match 56.7%; Score 10.2; DB 40; Length 43;
Best Local Similarity 80.0%; Pred. No. 9.4e+04;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AGCGTGCGCCATCCT 16
|| ||| |||||| |
Db 21 AGAGTGAGCCATCTT 35

RESULT 11
AA854777
LOCUS AA854777 46 bp mRNA EST 04-JAN-1999
DEFINITION aj77b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402443 3' similar to TR:Q14264 Q14264 ENVELOPE PROTEIN. ;contains LTR2.t3 LTR2 repetitive element ;, mRNA sequence.
ACCESSION AA854777
VERSION AA854777.1 GI:2942315
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 46)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2043498.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1357 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1402443"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'-
TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTTT
T-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid

adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
BASE COUNT 10 a 16 c 11 g 9 t
ORIGIN

Query Match 56.7%; Score 10.2; DB 39; Length 46;
Best Local Similarity 80.0%; Pred. No. 9.6e+04;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCGTGCGCCATCC 15
||||| | ||| |||
Db 31 CAGCGAGAGCCGTCC 45

RESULT 12
AA868659
LOCUS AA868659 31 bp mRNA EST 16-MAR-1998
DEFINITION ak49g02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409330 3' similar to TR:O14957 O14957 SMALLEST SUBUNIT OF UBIQUINOL-CYTOCHROME C REDUCTASE. ;, mRNA sequence.
ACCESSION AA868659
VERSION AA868659.1 GI:2964104
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2152319.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .31
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1409330"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 6 a 10 c 10 g 5 t
ORIGIN

Query Match 55.6%; Score 10; DB 39; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCGTGCGCC 11
||||||||||
Db 4 AGCGTGCGCC 13

RESULT 13
AA509356/c
LOCUS AA509356 41 bp mRNA EST 08-JUL-1997
DEFINITION vg18a09.r1 Soares mouse NbMH Mus musculus cDNA clone IMAGE:861688 5' similar to gb:M27034 Mouse MHC class I D-region cell surface antigen (MOUSE);, mRNA sequence.
ACCESSION AA509356
VERSION AA509356.1 GI:2247210
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 41)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1405263.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:505776
Trace considered overall poor quality
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .41
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:861688"
/clone_lib="Soares mouse NbMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGAAAGTTTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 4 a 13 c 16 g 8 t
ORIGIN

Query Match 55.6%; Score 10; DB 34; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CAGCGTGCGC 10
          ||||||||||
Db     29 CAGCGTGCGC 20


RESULT  14
AQ025518
LOCUS       AQ025518       45 bp    DNA             GSS       14-OCT-1998
DEFINITION  EP(X)1587 Drosophila melanogaster EP line Drosophila melanogaster
            genomic Sequence recovered from 5' end of P element, genomic survey
            sequence.
ACCESSION   AQ025518
VERSION     AQ025518.1  GI:3265870
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Rehm,E.J. and Rubin,G.M.
  TITLE     The BDGP gene disruption project: single EP element insertions
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Gerald Rubin
            Berkeley Drosophila Genome Project
            University of California, Berkeley
            LSA Building, Berkeley, CA 94720-3200, USA
            Fax: 5106439947
            Email: gerry@fruitfly.berkeley.edu

            Sequence recovery method was inverse PCR.

            Sequence orientation is forward strand relative to 5' end of P
            element

            The P element insertion position is base 38 in the 45 bases. This
            insertion position refers to the first base of the 8 base target
            recognition sequence.

            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="Drosophila melanogaster EP line"
                     /note="Inverse PCR was performed on Drosophila
                     melanogaster strains each of which contains a single EP
                     transposable element insertion. (The generation of these
                     insertion strains is described in Rorth P, Szabo K, Bailey
                     A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes
                     V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function
                     genetics in Drosophila. Development 6:1049-1057.) The
                     resultant fragment for each strain was directly sequenced
                     to determine the genomic sequence at the site of
                     insertion. Details of the protocols used can be found at
                     http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."
BASE COUNT        5 a     20 c      9 g     11 t
ORIGIN


  Query Match             55.6%;  Score 10;  DB 94;  Length 45;
  Best Local Similarity   72.2%;  Pred. No. 1.2e+05;
  Matches   13;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          || | | || ||||| ||
Db      4 CACCCTTCGTCATCCCTC 21


RESULT  15
AI254752/c
LOCUS       AI254752       49 bp    mRNA            EST       02-DEC-1998
DEFINITION  qt89f07.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:1962469 3'
            similar to SW:WASP_MOUSE P70315 WISKOTT-ALDRICH SYNDROME PROTEIN
            HOMOLOG ;contains element MSR1 repetitive element ;, mRNA sequence.
ACCESSION   AI254752
VERSION     AI254752.1  GI:3862277
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 19, 1998 this sequence version replaced gi:2045048.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 764   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1962469"
                     /clone_lib="NCI_CGAP_Co14"
                     /tissue_type="moderately-differentiated adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.7 kb. Life Technologies catalog #:
                     11531-019"
BASE COUNT        4 a     19 c     22 g      4 t
ORIGIN


  Query Match             55.6%;  Score 10;  DB 44;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 AGCGTGCGCC 11
          ||||||||||
Db     25 AGCGTGCGCC 16


Search completed: June 18, 2000, 20:38:40
Job time: 7500 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 18, 2000, 19:20:07 ; Search time 49.25 Seconds
(without alignments)
91.441 Million cell updates/sec

Title: PCT-US97-18348-1
Perfect score: 18
Sequence: 1 CAGCGTGCGCCATCCTTC 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 391736

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	1	V11591	Liposomal bcl-2 an
c 2	18	100.0	20	1	Q86649	Bcl-2 translation
3	18	100.0	20	1	V19651	Human bcl-2 antise
c 4	18	100.0	20	1	V19657	Human bcl-2 transc
5	18	100.0	22	1	Q49816	Bcl-2 antisense ol
6	18	100.0	22	1	Q49817	Bcl-2 antisense ol
c 7	18	100.0	35	1	Q86644	Bcl-2 translation
c 8	18	100.0	35	1	V19652	Human bcl-2 oligon
9	16	88.9	17	1	V19660	Human bcl-2 antise
10	16	88.9	17	1	V19661	Human bcl-2 antise
11	13	72.2	17	1	V19662	Human bcl-2 antise
12	13	72.2	17	1	V19659	Human bcl-2 antise
13	13	72.2	18	1	Q86659	Bcl-2 antisense ol
14	13	72.2	18	1	V19667	Human bcl-2 antise
15	13	72.2	18	1	V27719	Immunostimulatory
16	13	72.2	18	1	V28181	Antisense oligonuc
17	13	72.2	18	1	V52545	Unmethylated CpG d
18	13	72.2	18	1	V99434	Antisense oligonuc
19	13	72.2	18	1	X18702	Target bcl-2 antis
c 20	13	72.2	18	1	X27536	Synthetic RNA sequ
21	13	72.2	18	1	X23693	Deletion sequence
22	13	72.2	20	1	V74246	CpG-N motif SOS-OD
c 23	13	72.2	27	1	T18388	Human Bcl-2 forwar
24	12.8	71.1	24	1	T72509	Human papillomavir
25	12.4	68.9	45	1	T09247	nAChR beta2 subuni
26	12.2	67.8	30	1	T15239	Primer #2 for huma
27	12.2	67.8	30	1	V01975	Human myelin oligo
28	11.8	65.6	21	1	T97068	T84 target specifi
29	11.8	65.6	21	1	V02110	Human steroid 5-al
30	11.8	65.6	21	1	V02120	Human steroid 5-al
31	11.8	65.6	31	1	V14389	Primer Ps160 for c
c 32	11.8	65.6	35	1	Q99466	Human type I stero
33	11.8	65.6	40	1	T92291	Breast cancer tiss
c 34	11.8	65.6	45	1	Q99478	Human type I stero
c 35	11.8	65.6	45	1	T99818	Primer h5a35 for h
36	11.8	65.6	48	1	T30818	HDV ribozyme prime
37	11.8	65.6	48	1	V42395	Reverse PCR primer
38	11.8	65.6	48	1	V60155	Reverse PCR primer
39	11.8	65.6	48	1	V70715	Reverse primer SHD
40	11.6	64.4	28	1	T64675	Human PEC-60-type
41	11.4	63.3	18	1	V27733	Immunostimulatory
42	11.4	63.3	18	1	V52559	Unmethylated CpG d
43	11.4	63.3	18	1	V47681	Unmethylated CpG d
44	11.4	63.3	20	1	X09086	Tumour necrosis fa
45	11.4	63.3	25	1	Q48723	NEO gene primer 3.

ALIGNMENTS

RESULT 1
V11591
ID V11591 standard; DNA; 18 BP.
AC V11591;
DT 30-JUL-1998 (first entry)
DE Liposomal bcl-2 antisense polynucleotide.
KW Bcl-2; antisense; disease; treatment; cancer; follicular lymphoma;
KW leukaemia; plasma cell dyscrasia; breast; prostate; colon;
KW autoimmune diseases; ss.
OS Synthetic.
OS Homo sapiens.
PN WO9814172-A1.
PD 09-APR-1998.
PF 03-OCT-1997; U18348.
PR 04-OCT-1996; US-726211.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Lopez-Berestein G, McDonnel TJ, Tara AM, Tormo M;
DR WPI; 98-239841/21.
PT Composition comprising oligo:nucleotide anti-sense to Bcl-2 gene -
PT useful for, e.g. treatment of Bcl-2 related disease such as
PT follicular lymphoma and auto-immune disease
PS Claim 4; Page 30; 69pp; English.
CC This sequence is a nuclease-resistant p-ethoxy antisense oligonucleotide
CC which specifically binds to the translation initiation site of human
CC Bcl-2 mRNA. This oligonucleotide can be used in a method to treat Bcl-2
CC related disease in humans and animals, e.g. cancer especially follicular
CC lymphoma (FL), leukaemia, plasma cell dyscrasia, cancer of breast,
CC prostate and colon, or autoimmune diseases.
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T;

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCGTGCGCCATCCTTC 18
||||||||||||||||||
Db 1 CAGCGTGCGCCATCCTTC 18

RESULT 2
Q86649/c
ID Q86649 standard; DNA; 20 BP.
AC Q86649;
DT 27-SEP-1995 (first entry)
DE Bcl-2 translation initiation site region.
KW Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW lymphoma; programmed cell death; ss.
OS Synthetic.
PN WO9508350-A.
PD 30-MAR-1995.
PF 20-SEP-1994; U10725.
PR 20-SEP-1993; US-124256.
PA (REED/) REED J C.
PI Reed JC;
DR WPI; 95-139394/18.
PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

```
PT   of human solid tumours, esp. breast cancer
PS   Example 12; Page 33; 108pp; English.
CC   Antisense oligonucleotides were tested for their ability to induce
CC   programmed cell death (DNA fragmentation) in the human lymphoma cell
CC   line RS11846.  The oligonucleotides are phosphodiesters targeted
CC   against the translation initiation site (Q86650-55) or the 5'-cap
CC   region (Q86656-58) of human bcl-2 pre-mRNAs.  A bcl-2 sense sequence
CC   (Q86649) was used as a control.
SQ   Sequence   20 BP;    4 A;    4 C;    10 G;    2 T;


  Query Match            100.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.64;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     20 CAGCGTGCGCCATCCTTC 3


RESULT   3
V19651
ID   V19651 standard; DNA; 20 BP.
AC   V19651;
DT   12-JUN-1998  (first entry)
DE   Human bcl-2 antisense oligonucleotide 1.
KW   Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW   cancer; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   US5734033-A.
PD   31-MAR-1998.
PF   24-MAR-1994; 288692.
PR   21-FEB-1992; US-840716.
PR   22-DEC-1988; US-288692.
PR   24-MAR-1994; US-217082.
PA   (UYPE-) UNIV PENNSYLVANIA.
PI   Reed J;
DR   WPI; 98-229881/20.
PT   Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT   for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
PS   Claim 6; Columns 3-4; 21pp; English.
CC   This antisense oligonucleotide is complementary to the translation
CC   initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
CC   oligonucleotides are phosphorothioate derivatives and can straddle
CC   strategic sites such as the translation initiation site, donor and
CC   acceptor splicing sites, or sites for transportation or degradation.
CC   Blocking translation at such strategic sites prevents the formation of
CC   a functional bcl-2 gene product. These oligonucleotides may be used for
CC   treating cancers associated with high levels of bcl-2 gene expression,
CC   especially lymphomas and some leukaemias.
SQ   Sequence   20 BP;    2 A;    10 C;    4 G;    4 T;


  Query Match            100.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.64;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      1 CAGCGTGCGCCATCCTTC 18


RESULT   4
V19657/c
ID   V19657 standard; DNA; 20 BP.
AC   V19657;
DT   12-JUN-1998  (first entry)
DE   Human bcl-2 transcription initiation sense (TI-S) oligonucleotide.
KW   Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW   cancer; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   US5734033-A.
PD   31-MAR-1998.
PF   24-MAR-1994; 288692.
PR   21-FEB-1992; US-840716.
PR   22-DEC-1988; US-288692.
PR   24-MAR-1994; US-217082.
PA   (UYPE-) UNIV PENNSYLVANIA.
PI   Reed J;
DR   WPI; 98-229881/20.
PT   Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT   for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
PS   Disclosure; Column 19; 21pp; English.
CC   This oligonucleotide is used as a control in measuring DNA fragmentation
CC   as an indicator of bcl-2 antisense oligonucleotide mediated programmed
CC   cell death in human lymphoma cells. Bcl-2 antisense oligonucleotides
CC   straddle strategic sites such as the translation initiation site, donor
CC   and acceptor splicing sites, or sites for transportation or degradation.
CC   Blocking translation at such strategic sites prevents the formation of a
CC   functional bcl-2 gene product. These oligonucleotides may be used for
CC   treating cancers associated with high levels of bcl-2 gene expression,
CC   especially lymphomas and some leukaemias.
SQ   Sequence   20 BP;    4 A;    4 C;    10 G;    2 T;


  Query Match            100.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.64;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     20 CAGCGTGCGCCATCCTTC 3


RESULT   5
Q49816
ID   Q49816 standard; DNA; 22 BP.
AC   Q49816;
DT   03-MAY-1994  (first entry)
DE   Bcl-2 antisense oligonucleotide.
KW   Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW   expression; myc; ss.
OS   Synthetic.
PN   WO9320200-A.
PD   14-OCT-1993.
PF   02-APR-1993; G00686.
PR   02-APR-1992; GB-007275.
PR   02-APR-1992; GB-007276.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PI   Evan GI;
DR   WPI; 93-336908/42.
PT   Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT   esp. by inhibiting expression of the BCL-2 oncogene e.g. with
PT   antisense oligo:nucleotide(s), also increasing survival of
PT   cultured cells by expressing BCL-2
PS   Disclosure; Page 58; 109pp; English.
CC   A DNA construct comprising the bcl-2 coding sequence under control
CC   of elements allowing its expression is claimed.  Myc-induced cell
CC   death can be inhibited in cultured cells by expressing bcl-2.
CC   Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC   of bcl-2 antisense oligonucleotides.
SQ   Sequence   22 BP;    2 A;    12 C;    4 G;    4 T;


  Query Match            100.0%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.64;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      3 CAGCGTGCGCCATCCTTC 20


RESULT   6
```

```
Q49817
ID   Q49817 standard; RNA; 22 BP.
AC   Q49817;
DT   03-MAY-1994  (first entry)
DE   Bcl-2 antisense oligonucleotide.
KW   Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW   expression; myc; ss.
OS   Synthetic.
PN   WO9320200-A.
PD   14-OCT-1993.
PF   02-APR-1993; G00686.
PR   02-APR-1992; GB-007275.
PR   02-APR-1992; GB-007276.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PI   Evan GI;
DR   WPI; 93-336908/42.
PT   Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT   esp. by inhibiting expression of the BCL-2 oncogene e.g. with
PT   antisense oligo:nucleotide(s), also increasing survival of
PT   cultured cells by expressing BCL-2
PS   Disclosure; Page 58; 109pp; English.
CC   A DNA construct comprising the bcl-2 coding sequence under control
CC   of elements allowing its expression is claimed.  Myc-induced cell
CC   death can be inhibited in cultured cells by expressing bcl-2.
CC   Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC   of bcl-2 antisense oligonucleotides.
SQ   Sequence   22 BP;    2 A;    12 C;    4 G;    4 U;


  Query Match            100.0%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   77.8%;  Pred. No. 0.64;
  Matches   14;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          |||||:||||||:||::|
Db      3 CAGCGUGCGCCAUCCUUC 20


RESULT   7
Q86644/c
ID   Q86644 standard; DNA; 35 BP.
AC   Q86644;
DT   27-SEP-1995  (first entry)
DE   Bcl-2 translation initiation region.
KW   Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW   leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
KW   ss.
OS   Synthetic.
PN   WO9508350-A.
PD   30-MAR-1995.
PF   20-SEP-1994; U10725.
PR   20-SEP-1993; US-124256.
PA   (REED/) REED J C.
PI   Reed JC;
DR   WPI; 95-139394/18.
PT   Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT   of human solid tumours, esp. breast cancer
PS   Disclosure; Page 13; 108pp; English.
CC   The antisense oligonucleotide TI-AS (Q86643) straddles the
CC   translation-initiation site in the mRNA coding strand of the human
CC   bcl-2 gene and is complementary to this region.  It reduces the
CC   expression of bcl-2 gene product thereby inducing programmed cell
CC   death of certain cancer cells.  The corresp. sense bcl-1 sequence
CC   was synthesized for use as a control.
SQ   Sequence   35 BP;    6 A;    8 C;    13 G;    8 T;


  Query Match            100.0%;  Score 18;  DB 1;  Length 35;
  Best Local Similarity  100.0%;  Pred. No. 0.66;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     30 CAGCGTGCGCCATCCTTC 13


RESULT   8
V19652/c
ID   V19652 standard; DNA; 35 BP.
AC   V19652;
DT   12-JUN-1998  (first entry)
DE   Human bcl-2 oligonucleotide 1.
KW   Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW   cancer; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   US5734033-A.
PD   31-MAR-1998.
PF   24-MAR-1994; 288692.
PR   21-FEB-1992; US-840716.
PR   22-DEC-1988; US-288692.
PR   24-MAR-1994; US-217082.
PA   (UYPE-) UNIV PENNSYLVANIA.
PI   Reed J;
DR   WPI; 98-229881/20.
PT   Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT   for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
PS   Claim 1; Columns 3-4; 21pp; English.
CC   This is a human bcl-2 oligonucleotide based on which an antisense
CC   oligonucleotide complementary to the translation initiation site of the
CC   human bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides
CC   straddle strategic sites such as the translation initiation site, donor
CC   and acceptor splicing sites, or sites for transportation or degradation.
CC   Blocking translation at such strategic sites prevents the formation of a
CC   functional bcl-2 gene product. These oligonucleotides may be used for
CC   treating cancers associated with high levels of bcl-2 gene expression,
CC   especially lymphomas and some leukaemias.
SQ   Sequence   35 BP;    6 A;    8 C;    13 G;    8 T;


  Query Match            100.0%;  Score 18;  DB 1;  Length 35;
  Best Local Similarity  100.0%;  Pred. No. 0.66;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     30 CAGCGTGCGCCATCCTTC 13


RESULT   9
V19660
ID   V19660 standard; DNA; 17 BP.
AC   V19660;
DT   12-JUN-1998  (first entry)
DE   Human bcl-2 antisense oligonucleotide 6.
KW   Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW   cancer; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   US5734033-A.
PD   31-MAR-1998.
PF   24-MAR-1994; 288692.
PR   21-FEB-1992; US-840716.
PR   22-DEC-1988; US-288692.
PR   24-MAR-1994; US-217082.
PA   (UYPE-) UNIV PENNSYLVANIA.
PI   Reed J;
DR   WPI; 98-229881/20.
PT   Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT   for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
PS   Claim 6; Column 14; 21pp; English.
CC   This antisense oligonucleotide is complementary to the translation
CC   initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
CC   oligonucleotides are phosphorothioate derivatives and can straddle
CC   strategic sites such as the translation initiation site, donor and
CC   acceptor splicing sites, or sites for transportation or degradation.
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CC   Blocking translation at such strategic sites prevents the formation of
CC   a functional bcl-2 gene product. These oligonucleotides may be used for
CC   treating cancers associated with high levels of bcl-2 gene expression,
CC   especially lymphomas and some leukaemias.
SQ   Sequence   17 BP;    2 A;    8 C;    4 G;    3 T;


  Query Match             88.9%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.9;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCT 16
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Db      2 CAGCGTGCGCCATCCT 17


RESULT  10
V19661
ID   V19661 standard; DNA; 17 BP.
AC   V19661;
DT   12-JUN-1998  (first entry)
DE   Human bcl-2 antisense oligonucleotide 7.
KW   Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW   cancer; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   US5734033-A.
PD   31-MAR-1998.
PF   24-MAR-1994; 288692.
PR   21-FEB-1992; US-840716.
PR   22-DEC-1988; US-288692.
PR   24-MAR-1994; US-217082.
PA   (UYPE-) UNIV PENNSYLVANIA.
PI   Reed J;
DR   WPI; 98-229881/20.
PT   Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT   for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
PS   Disclosure; Column 14; 21pp; English.
CC   This antisense oligonucleotide is complementary to the translation
CC   initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
CC   oligonucleotides are phosphorothioate derivatives and can straddle
CC   strategic sites such as the translation initiation site, donor and
CC   acceptor splicing sites, or sites for transportation or degradation.
CC   Blocking translation at such strategic sites prevents the formation of
CC   a functional bcl-2 gene product. These oligonucleotides may be used for
CC   treating cancers associated with high levels of bcl-2 gene expression,
CC   especially lymphomas and some leukaemias.
SQ   Sequence   17 BP;    1 A;    8 C;    4 G;    4 T;


  Query Match             88.9%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.9;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCGTGCGCCATCCTTC 18
          ||||||||||||||||
Db      1 GCGTGCGCCATCCTTC 16


RESULT  11
V19662
ID   V19662 standard; DNA; 17 BP.
AC   V19662;
DT   12-JUN-1998  (first entry)
DE   Human bcl-2 antisense oligonucleotide 8.
KW   Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW   cancer; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   US5734033-A.
PD   31-MAR-1998.
PF   24-MAR-1994; 288692.
PR   21-FEB-1992; US-840716.
PR   22-DEC-1988; US-288692.
PR   24-MAR-1994; US-217082.
PA   (UYPE-) UNIV PENNSYLVANIA.
PI   Reed J;
DR   WPI; 98-229881/20.
PT   Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT   for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
PS   Disclosure; Column 14; 21pp; English.
CC   This antisense oligonucleotide is complementary to the translation
CC   initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
CC   oligonucleotides are phosphorothioate derivatives and can straddle
CC   strategic sites such as the translation initiation site, donor and
CC   acceptor splicing sites, or sites for transportation or degradation.
CC   Blocking translation at such strategic sites prevents the formation of
CC   a functional bcl-2 gene product. These oligonucleotides may be used for
CC   treating cancers associated with high levels of bcl-2 gene expression,
CC   especially lymphomas and some leukaemias.
SQ   Sequence   17 BP;    2 A;    8 C;    3 G;    4 T;


  Query Match             72.2%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 TGCGCCATCCTTC 18
          |||||||||||||
Db      1 TGCGCCATCCTTC 13


RESULT  12
V19659
ID   V19659 standard; DNA; 17 BP.
AC   V19659;
DT   12-JUN-1998  (first entry)
DE   Human bcl-2 antisense oligonucleotide 5.
KW   Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW   cancer; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   US5734033-A.
PD   31-MAR-1998.
PF   24-MAR-1994; 288692.
PR   21-FEB-1992; US-840716.
PR   22-DEC-1988; US-288692.
PR   24-MAR-1994; US-217082.
PA   (UYPE-) UNIV PENNSYLVANIA.
PI   Reed J;
DR   WPI; 98-229881/20.
PT   Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT   for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
PS   Claim 6; Column 14; 21pp; English.
CC   This antisense oligonucleotide is complementary to the translation
CC   initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
CC   oligonucleotides are phosphorothioate derivatives and can straddle
CC   strategic sites such as the translation initiation site, donor and
CC   acceptor splicing sites, or sites for transportation or degradation.
CC   Blocking translation at such strategic sites prevents the formation of
CC   a functional bcl-2 gene product. These oligonucleotides may be used for
CC   treating cancers associated with high levels of bcl-2 gene expression,
CC   especially lymphomas and some leukaemias.
SQ   Sequence   17 BP;    2 A;    8 C;    4 G;    3 T;


  Query Match             72.2%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCAT 13
          |||||||||||||
Db      5 CAGCGTGCGCCAT 17


RESULT  13
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Q86659
ID   Q86659 standard; DNA; 18 BP.
AC   Q86659;
DT   27-SEP-1995  (first entry)
DE   Bcl-2 antisense oligonucleotide.
KW   Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW   chemoresistance; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   misc_feature    1. .18
FT                   /*tag= a
FT                   /note= "3'-5' (antisense) sequence"
PN   WO9508350-A.
PD   30-MAR-1995.
PF   20-SEP-1994; U10725.
PR   20-SEP-1993; US-124256.
PA   (REED/) REED J C.
PI   Reed JC;
DR   WPI; 95-139394/18.
PT   Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT   of human solid tumours, esp. breast cancer
PS   Example 18; Page 44; 108pp; English.
CC   Reversal of chemoresistance of tumor cells by antisense-mediated
CC   reduction of bcll-2 expression was demonstrated using the
CC   oligonucleotide given in Q86659.  This is antisense to the first
CC   6 codons of the bcl-2 ORF.
SQ   Sequence   18 BP;    2 A;    8 C;    4 G;    4 T;


  Query Match             72.2%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCAT 13
          |||||||||||||
Db      6 CAGCGTGCGCCAT 18


RESULT  14
V19667
ID   V19667 standard; DNA; 18 BP.
AC   V19667;
DT   12-JUN-1998  (first entry)
DE   Human bcl-2 antisense oligonucleotide 13.
KW   Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW   cancer; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   US5734033-A.
PD   31-MAR-1998.
PF   24-MAR-1994; 288692.
PR   21-FEB-1992; US-840716.
PR   22-DEC-1988; US-288692.
PR   24-MAR-1994; US-217082.
PA   (UYPE-) UNIV PENNSYLVANIA.
PI   Reed J;
DR   WPI; 98-229881/20.
PT   Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT   for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
PS   Disclosure; Column 23; 21pp; English.
CC   This antisense oligonucleotide is complementary to the translation
CC   initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
CC   oligonucleotides are phosphorothioate derivatives and can straddle
CC   strategic sites such as the translation initiation site, donor and
CC   acceptor splicing sites, or sites for transportation or degradation.
CC   Blocking translation at such strategic sites prevents the formation of
CC   a functional bcl-2 gene product. These oligonucleotides may be used for
CC   treating cancers associated with high levels of bcl-2 gene expression,
CC   especially lymphomas and some leukaemias.
SQ   Sequence   18 BP;    2 A;    8 C;    4 G;    4 T;


  Query Match             72.2%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCAT 13
          |||||||||||||
Db      6 CAGCGTGCGCCAT 18


RESULT  15
V27719
ID   V27719 standard; DNA; 18 BP.
AC   V27719;
DT   01-OCT-1998  (first entry)
DE   Immunostimulatory oligodeoxyribonucleotide of the invention.
KW   Immunostimulatory; oligodeoxyribonucleotide; ODN;
KW   unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
KW   Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
KW   desensitisation therapy; artificial adjuvant; antibody generation; ss.
OS   Synthetic.
PN   WO9818810-A1.
PD   07-MAY-1998.
PF   30-OCT-1997; U19791.
PR   30-OCT-1996; US-738652.
PA   (IOWA ) UNIV IOWA RES FOUND.
PI   Kline JN, Krieg AM;
DR   WPI; 98-272127/24.
PT   New immunostimulatory nucleic acid molecules - which contain at
PT   least one unmethylated CpG dinucleotide, used for treating e.g.
PT   tumours, infections or autoimmune disease
PS   Disclosure; Page 49; 109pp; English.
CC   V27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs)
CC   of the invention. The ODNs contain at least one unmethylated CpG
CC   dinucleotide, and have the formula:
CC   5' N1X1CGX2N2 3', where at least one nucleotide separates consecutive
CC   CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N is
CC   any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2
CC   does not contain a CCGG tetramer or more than one CCG or CGG trimer OR
CC   5' NX1X2CGX3X4N 3', where at least one nucleotide separates consecutive
CC   CpGs, X1 and X2 are selected from GpT, GpG, GpA, ApT and ApA, X3and X4
CC   are selected from TpT or CpT, N is any nucleotide and N1+N2 is 0-26
CC   bases with the provision that N1 and N2 does not contain a CCGG tetramer
CC   or more than one CCG or CGG trimer.
CC   The ODNs activate lymphocytes in a subject and redirect a subject's
CC   immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells and
CC   other cells to produce Th1 cytokines, including IL-12, IFN-gamma and
CC   GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder,
CC   autoimmune diseases, in desensitisation therapy, as an artificial
CC   adjuvant during antibody generation in a mammal such as a mouse or a
CC   human.
SQ   Sequence   18 BP;    2 A;    8 C;    4 G;    4 T;


  Query Match             72.2%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCAT 13
          |||||||||||||
Db      6 CAGCGTGCGCCAT 18


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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: PCT-US97-18348-1
Perfect score: 18
Sequence: 1 CAGCGTGCGCCATCCTTC 18

Scoring table: IDENTITY_NUC
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Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 285916

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Listing first 45 summaries

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58: gb_htg14:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	20	5	AR052603	AR052603 Sequence
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	3	18	100.0	20	5	I96082	I96082 Sequence 1
c	4	18	100.0	20	5	I96088	I96088 Sequence 7
	5	18	100.0	22	5	A76123	A76123 Sequence 3
	6	18	100.0	22	5	A76124	A76124 Sequence 4
c	7	18	100.0	35	5	AR052604	AR052604 Sequence
c	8	18	100.0	35	5	I96083	I96083 Sequence 2
	9	16	88.9	17	5	I96091	I96091 Sequence 10
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	13	13	72.2	17	5	I96093	I96093 Sequence 12
	14	13	72.2	18	5	AR052619	AR052619 Sequence
	15	13	72.2	18	5	AR052624	AR052624 Sequence
	16	13	72.2	18	5	I96098	I96098 Sequence 17
c	17	13	72.2	27	5	AR004426	AR004426 Sequence
c	18	13	72.2	27	5	I43661	I43661 Sequence 13
c	19	13	72.2	27	5	I86720	I86720 Sequence 8
c	20	11.8	65.6	25	5	I09491	I09491 Sequence 5
c	21	11.8	65.6	45	5	I12347	I12347 Sequence 36
c	22	11.8	65.6	45	5	I70250	I70250 Sequence 36
	23	11.8	65.6	48	5	AR021008	AR021008 Sequence
	24	11.8	65.6	48	5	AR043423	AR043423 Sequence
	25	11.8	65.6	48	5	AR062338	AR062338 Sequence
	26	11	61.1	31	5	AR041195	AR041195 Sequence
	27	10.8	60.0	17	5	I46922	I46922 Sequence 15
	28	10.8	60.0	21	5	A98631	A98631 Sequence 25
c	29	10.8	60.0	26	24	E11773	E11773 Synthetic o
c	30	10.8	60.0	35	5	I15202	I15202 Sequence 19
	31	10.8	60.0	35	5	I15205	I15205 Sequence 22
c	32	10.8	60.0	36	5	A26295	A26295 Subtilisin
	33	10.8	60.0	36	5	A26296	A26296 Subtilisin
c	34	10.8	60.0	36	5	A26927	A26927 oligonucleo
	35	10.8	60.0	36	5	A26928	A26928 oligonucleo
c	36	10.8	60.0	36	5	I43384	I43384 Sequence 13
	37	10.8	60.0	36	5	I43385	I43385 Sequence 14
c	38	10.6	58.9	20	5	A51364	A51364 Sequence 6
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c	41	10.6	58.9	33	5	AR008552	AR008552 Sequence
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c	45	10.6	58.9	50	5	A25419	A25419 oligonucleo

ALIGNMENTS

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LOCUS       AR052603       20 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 1 from patent US 5831066.
ACCESSION   AR052603
VERSION     AR052603.1  GI:5975967
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 1 03-NOV-1998;
FEATURES             Location/Qualifiers
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BASE COUNT        2 a      10 c      4 g      4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 41;
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Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      1 CAGCGTGCGCCATCCTTC 18


RESULT   2
AR052609/c
LOCUS       AR052609       20 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 7 from patent US 5831066.
ACCESSION   AR052609
VERSION     AR052609.1  GI:5975973
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 7 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      4 c      10 g      2 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     20 CAGCGTGCGCCATCCTTC 3


RESULT   3
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LOCUS       I96082         20 bp    DNA             PAT       01-DEC-1998
DEFINITION  Sequence 1 from patent US 5734033.
ACCESSION   I96082
VERSION     I96082.1  GI:3940552
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Reed,J.
  TITLE     Antisense oligonucleotides inhibiting human bcl-2 gene expression
  JOURNAL   Patent: US 5734033-A 1 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .20
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BASE COUNT        2 a      10 c      4 g      4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      1 CAGCGTGCGCCATCCTTC 18


RESULT   4
I96088/c
LOCUS       I96088         20 bp    DNA             PAT       01-DEC-1998
DEFINITION  Sequence 7 from patent US 5734033.
ACCESSION   I96088
VERSION     I96088.1  GI:3940558
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Reed,J.
  TITLE     Antisense oligonucleotides inhibiting human bcl-2 gene expression
  JOURNAL   Patent: US 5734033-A 7 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      4 c      10 g      2 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     20 CAGCGTGCGCCATCCTTC 3


RESULT   5
A76123
LOCUS       A76123         22 bp    DNA             PAT       19-OCT-1999
DEFINITION  Sequence 3 from Patent WO9320200.
ACCESSION   A76123
VERSION     A76123.1  GI:6088259
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Evan,G.I.
  TITLE     MODIFIED CELLS AND METHOD OF TREATMENT
  JOURNAL   Patent: WO 9320200-A 14-OCT-1993;
            IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      12 c      4 g      4 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 41;
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  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
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Db      3 CAGCGTGCGCCATCCTTC 20


RESULT   6
A76124
LOCUS       A76124          22 bp    DNA             PAT       19-OCT-1999
DEFINITION  Sequence 4 from Patent WO9320200.
ACCESSION   A76124
VERSION     A76124.1  GI:6088260
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Evan,G.I.
  TITLE     MODIFIED CELLS AND METHOD OF TREATMENT
  JOURNAL   Patent: WO 9320200-A 14-OCT-1993;
            IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      12 c       4 g       4 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db      3 CAGCGTGCGCCATCCTTC 20


RESULT   7
AR052604/c
LOCUS       AR052604        35 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 2 from patent US 5831066.
ACCESSION   AR052604
VERSION     AR052604.1  GI:5975968
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 2 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT        6 a      8 c      13 g      8 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     30 CAGCGTGCGCCATCCTTC 13


RESULT   8
I96083/c
LOCUS       I96083          35 bp    DNA             PAT       01-DEC-1998
DEFINITION  Sequence 2 from patent US 5734033.
ACCESSION   I96083
VERSION     I96083.1  GI:3940553
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Reed,J.
  TITLE     Antisense oligonucleotides inhibiting human bcl-2 gene expression
  JOURNAL   Patent: US 5734033-A 2 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT        6 a      8 c      13 g      8 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCTTC 18
          ||||||||||||||||||
Db     30 CAGCGTGCGCCATCCTTC 13


RESULT   9
I96091
LOCUS       I96091          17 bp    DNA             PAT       01-DEC-1998
DEFINITION  Sequence 10 from patent US 5734033.
ACCESSION   I96091
VERSION     I96091.1  GI:3940561
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Reed,J.
  TITLE     Antisense oligonucleotides inhibiting human bcl-2 gene expression
  JOURNAL   Patent: US 5734033-A 10 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        2 a      8 c      4 g       3 t
ORIGIN


  Query Match             88.9%;  Score 16;  DB 5;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCATCCT 16
          ||||||||||||||||
Db      2 CAGCGTGCGCCATCCT 17


RESULT  10
I96092
LOCUS       I96092          17 bp    DNA             PAT       01-DEC-1998
DEFINITION  Sequence 11 from patent US 5734033.
ACCESSION   I96092
VERSION     I96092.1  GI:3940562
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Reed,J.
  TITLE     Antisense oligonucleotides inhibiting human bcl-2 gene expression
  JOURNAL   Patent: US 5734033-A 11 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
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BASE COUNT        1 a      8 c      4 g      4 t
ORIGIN


  Query Match             88.9%;  Score 16;  DB 5;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCGTGCGCCATCCTTC 18
           ||||||||||||||||
Db       1 GCGTGCGCCATCCTTC 16


RESULT  11
CHKC2A101/c
LOCUS       CHKC2A101      29 bp    DNA             VRT       23-MAY-1996
DEFINITION  Chicken alpha-1 type-II collagen gene; amino acids 578 to 585.
ACCESSION   K02260
VERSION     K02260.1  GI:211336
KEYWORDS    alpha-1 type II collagen; collagen.
SEGMENT     1 of 6
SOURCE      Gallus gallus (clone:  LgCOL(II).) DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
            Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Sandell,L.J., Yamada,Y., Dorfman,A. and Upholt,W.B.
  TITLE     Identification of genomic DNA coding for chicken type II
            procollagen
  JOURNAL   J. Biol. Chem. 258 (19), 11617-11621 (1983)
  MEDLINE   84008159
COMMENT     Each procollagen gene codes for the six successive functional
            regions of the protein:  signal peptide, NH-2 propeptide, NH-2
            telopeptide, helical peptide, COOH telopeptide, and COOH
            propeptide.  The type-II COOH-propeptide is cleaved from the
            procollagen molecule after the triple helical molecule is secreted
            into the extracellular matrix.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Gallus gallus"
                     /db_xref="taxon:9031"
                     /clone="LgCOL(II)."
                     /cell_type="reticulocyte"
     exon            <1. .24
                     /note="preprocollagen alpha-1 type-II, AA 578 to 585"
     intron          25. .>29
                     /note="collagen intron"
BASE COUNT        7 a      7 c     11 g      4 t
ORIGIN      Downstream of EcoRI site.


  Query Match             77.8%;  Score 14;  DB 4;  Length 29;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 CGTGCGCCATCCTT 17
           ||||||||||||||
Db      23 CGTGCGCCATCCTT 10


RESULT  12
I96090
LOCUS       I96090         17 bp    DNA             PAT       01-DEC-1998
DEFINITION  Sequence 9 from patent US 5734033.
ACCESSION   I96090
VERSION     I96090.1  GI:3940560
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Reed,J.
  TITLE     Antisense oligonucleotides inhibiting human bcl-2 gene expression
  JOURNAL   Patent: US 5734033-A 9 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        2 a      8 c      4 g      3 t
ORIGIN


  Query Match             72.2%;  Score 13;  DB 5;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCAT 13
           |||||||||||||
Db       5 CAGCGTGCGCCAT 17


RESULT  13
I96093
LOCUS       I96093         17 bp    DNA             PAT       01-DEC-1998
DEFINITION  Sequence 12 from patent US 5734033.
ACCESSION   I96093
VERSION     I96093.1  GI:3940563
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Reed,J.
  TITLE     Antisense oligonucleotides inhibiting human bcl-2 gene expression
  JOURNAL   Patent: US 5734033-A 12 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        2 a      8 c      3 g      4 t
ORIGIN


  Query Match             72.2%;  Score 13;  DB 5;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 TGCGCCATCCTTC 18
           |||||||||||||
Db       1 TGCGCCATCCTTC 13


RESULT  14
AR052619
LOCUS       AR052619       18 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 17 from patent US 5831066.
ACCESSION   AR052619
VERSION     AR052619.1  GI:5975983
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 17 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      8 c      4 g      4 t
ORIGIN


  Query Match             72.2%;  Score 13;  DB 5;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAGCGTGCGCCAT 13
```

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          ||||||||||||
Db      6 CAGCGTGCGCCAT 18


RESULT  15
AR052624
LOCUS       AR052624       18 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 24 from patent US 5831066.
ACCESSION   AR052624
VERSION     AR052624.1  GI:5975988
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 24 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      8 c      4 g      4 t
ORIGIN


  Query Match             72.2%;  Score 13;  DB 5;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGCGTGCGCCAT 13
          |||||||||||||
Db      6 CAGCGTGCGCCAT 18


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